



SEQUENCE LISTING

<110> DEREK O'HAGAN
MICHAEL HOUGHTON
MANMOHAN SINGH

<120> COMPOSITIONS COMPRISING CATIONIC MICROPARTICLES
AND HCV E1E2 DNA AND METHODS OF USE THEREOF

<130> PP020407.0004

<140> 10/554,625

<141> 2007-03-21

<150> 60/465,841

<151> 2003-04-25

<160> 2

<170> PatentIn Ver. 2.0

<210> 1

<211> 1914

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HCV-1 E1/E2/p7 region

<220>

<221> CDS

<222> (1)..(1911)

<400> 1

tct	ttc	tct	atc	ttc	ctt	ctg	gcc	ctg	ctc	tct	tgc	ttg	act	gtg	ccc	48
Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	
1				5					10					15		

gct	tcg	gcc	tac	caa	gtg	cgc	aac	tcc	acg	ggg	ctc	tac	cac	gtc	acc	96
Ala	Ser	Ala	Tyr	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	
			20					25					30			

aat	gat	tgc	cct	aac	tcg	agt	att	gtg	tac	gag	gcg	gcc	gat	gcc	atc	144
Asn	Asp	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	
		35					40					45				

ctg	cac	act	ccg	ggg	tgc	gtc	cct	tgc	gtt	cgc	gag	ggc	aac	gcc	tcg	192
Leu	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ala	Ser	
	50					55					60					

agg	tgt	tgg	gtg	gcg	atg	acc	cct	acg	gtg	gcc	acc	agg	gat	ggc	aaa	240
Arg	Cys	Trp	Val	Ala	Met	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly	Lys	
65					70				75					80		

ctc	ccc	gcg	acg	cag	ctt	cga	cgt	cac	atc	gat	ctg	ctt	gtc	ggg	agc	288
Leu	Pro	Ala	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val	Gly	Ser	
				85				90						95		

gcc	acc	ctc	tgt	tcg	gcc	ctc	tac	gtg	ggg	gac	ctg	tgc	ggg	tct	gtc	336
Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Ser	Val	

100						105						110						
ttt	ctt	gtc	ggc	caa	ctg	ttt	acc	ttc	tct	ccc	agg	cgc	cac	tgg	acg	384		
Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	Arg	His	Trp	Thr			
		115					120					125						
acg	caa	ggt	tgc	aat	tgc	tct	atc	tat	ccc	ggc	cat	ata	acg	ggt	cac	432		
Thr	Gln	Gly	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His			
	130					135					140							
cgc	atg	gca	tgg	gat	atg	atg	atg	aac	tgg	tcc	cct	acg	acg	gcg	ttg	480		
Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu			
145					150					155					160			
gta	atg	gct	cag	ctg	ctc	cgg	atc	cca	caa	gcc	atc	ttg	gac	atg	atc	528		
Val	Met	Ala	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Ile	Leu	Asp	Met	Ile			
				165					170					175				
gct	ggt	gct	cac	tgg	gga	gtc	ctg	gcg	ggc	ata	gcg	tat	ttc	tcc	atg	576		
Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met			
			180					185					190					
gtg	ggg	aac	tgg	gcg	aag	gtc	ctg	gta	gtg	ctg	ctg	cta	ttt	gcc	ggc	624		
Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	Val	Leu	Leu	Leu	Phe	Ala	Gly			
		195					200					205						
gtc	gac	gcg	gaa	acc	cac	gtc	acc	ggg	gga	agt	gcc	ggc	cac	act	gtg	672		
Val	Asp	Ala	Glu	Thr	His	Val	Thr	Gly	Gly	Ser	Ala	Gly	His	Thr	Val			
	210					215					220							
tct	gga	ttt	gtt	agc	ctc	ctc	gca	cca	ggc	gcc	aag	cag	aac	gtc	cag	720		
Ser	Gly	Phe	Val	Ser	Leu	Leu	Ala	Pro	Gly	Ala	Lys	Gln	Asn	Val	Gln			
225					230					235					240			
ctg	atc	aac	acc	aac	ggc	agt	tgg	cac	ctc	aat	agc	acg	gcc	ctg	aac	768		
Leu	Ile	Asn	Thr	Asn	Gly	Ser	Trp	His	Leu	Asn	Ser	Thr	Ala	Leu	Asn			
				245					250					255				
tgc	aat	gat	agc	ctc	aac	acc	ggc	tgg	ttg	gca	ggg	ctt	ttc	tat	cac	816		
Cys	Asn	Asp	Ser	Leu	Asn	Thr	Gly	Trp	Leu	Ala	Gly	Leu	Phe	Tyr	His			
			260					265					270					
cac	aag	ttc	aac	tct	tca	ggc	tgt	cct	gag	agg	cta	gcc	agc	tgc	cga	864		
His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys	Arg			
		275					280					285						
ccc	ctt	acc	gat	ttt	gac	cag	ggc	tgg	ggc	cct	atc	agt	tat	gcc	aac	912		
Pro	Leu	Thr	Asp	Phe	Asp	Gln	Gly	Trp	Gly	Pro	Ile	Ser	Tyr	Ala	Asn			
		290				295					300							
gga	agc	ggc	ccc	gac	cag	cgc	ccc	tac	tgc	tgg	cac	tac	ccc	cca	aaa	960		
Gly	Ser	Gly	Pro	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Pro	Pro	Lys			
305					310					315					320			
cct	tgc	ggt	att	gtg	ccc	gcg	aag	agt	gtg	tgt	ggt	ccg	gta	tat	tgc	1008		
Pro	Cys	Gly	Ile	Val	Pro	Ala	Lys	Ser	Val	Cys	Gly	Pro	Val	Tyr	Cys			
				325					330					335				
ttc	act	ccc	agc	ccc	gtg	gtg	gtg	gga	acg	acc	gac	agg	tcg	ggc	gcg	1056		
Phe	Thr	Pro	Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Ser	Gly	Ala			

340	345	350	
ccc acc tac agc tgg ggt gaa aat gat acg gac gtc ttc gtc ctt aac Pro Thr Tyr Ser Trp Gly Glu Asn Asp Thr Asp Val Phe Val Leu Asn 355 360 365			1104
aat acc agg cca ccg ctg ggc aat tgg ttc ggt tgt acc tgg atg aac Asn Thr Arg Pro Pro Leu Gly Asn Trp Phe Gly Cys Thr Trp Met Asn 370 375 380			1152
tca act gga ttc acc aaa gtg tgc gga gcg cct cct tgt gtc atc gga Ser Thr Gly Phe Thr Lys Val Cys Gly Ala Pro Pro Cys Val Ile Gly 385 390 400			1200
ggg gcg ggc aac aac acc ctg cac tgc ccc act gat tgc ttc cgc aag Gly Ala Gly Asn Asn Thr Leu His Cys Pro Thr Asp Cys Phe Arg Lys 405 410 415			1248
cat ccg gac gcc aca tac tct cgg tgc ggc tcc ggt ccc tgg atc aca His Pro Asp Ala Thr Tyr Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr 420 425 430			1296
ccc agg tgc ctg gtc gac tac ccg tat agg ctt tgg cat tat cct tgt Pro Arg Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys 435 440 445			1344
acc atc aac tac act ata ttt aaa atc agg atg tac gtg gga ggg gtc Thr Ile Asn Tyr Thr Ile Phe Lys Ile Arg Met Tyr Val Gly Gly Val 450 455 460			1392
gag cac agg ctg gaa gct gcc tgc aac tgg acg cgg ggc gaa cgt tgc Glu His Arg Leu Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys 465 470 475 480			1440
gat ctg gaa gat agg gac agg tcc gag ctc agc ccg tta ctg ctg acc Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Thr 485 490 495			1488
act aca cag tgg cag gtc ctc ccg tgt tcc ttc aca acc ctg cca gcc Thr Thr Gln Trp Gln Val Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala 500 505 510			1536
ttg tcc acc ggc ctc atc cac ctc cac cag aac att gtg gac gtg cag Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln 515 520 525			1584
tac ttg tac ggg gtg ggg tca agc atc gcg tcc tgg gcc att aag tgg Tyr Leu Tyr Gly Val Gly Ser Ser Ile Ala Ser Trp Ala Ile Lys Trp 530 535 540			1632
gag tac gtc gtc ctc ctg ttc ctt ctg ctt gca gac gcg cgc gtc tgc Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys 545 550 555 560			1680
tcc tgc ttg tgg atg atg cta ctc ata tcc caa gcg gaa gcg gct ttg Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu Ala Ala Leu 565 570 575			1728
gag aac ctc gta ata ctt aat gca gca tcc ctg gcc ggg acg cac ggt Glu Asn Leu Val Ile Leu Asn Ala Ala Ser Leu Ala Gly Thr His Gly 580 585 590			1776

ctt gta tcc ttc ctc gtg ttc ttc tgc ttt gca tgg tat ctg aag ggt 1824
 Leu Val Ser Phe Leu Val Phe Phe Cys Phe Ala Trp Tyr Leu Lys Gly
 595 600 605

aag tgg gtg ccc gga gcg gtc tac acc ttc tac ggg atg tgg cct ctc 1872
 Lys Trp Val Pro Gly Ala Val Tyr Thr Phe Tyr Gly Met Trp Pro Leu
 610 615 620

ctc ctg ctc ctg ttg gcg ttg ccc cag cgg gcg tac gcg taa 1914
 Leu Leu Leu Leu Leu Ala Leu Pro Gln Arg Ala Tyr Ala
 625 630 635

<210> 2

<211> 637

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HCV-1 E1/E2/p7 region

<400> 2

Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro
 1 5 10 15

Ala Ser Ala Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr
 20 25 30

Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile
 35 40 45

Leu His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
 50 55 60

Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys
 65 70 75 80

Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser
 85 90 95

Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ser Val
 100 105 110

Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr
 115 120 125

Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His
 130 135 140

Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu
 145 150 155 160

Val Met Ala Gln Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile
 165 170 175

Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met
 180 185 190

Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu Leu Phe Ala Gly

195						200						205					
Val	Asp	Ala	Glu	Thr	His	Val	Thr	Gly	Gly	Ser	Ala	Gly	His	Thr	Val		
210						215					220						
Ser	Gly	Phe	Val	Ser	Leu	Leu	Ala	Pro	Gly	Ala	Lys	Gln	Asn	Val	Gln		
225					230					235					240		
Leu	Ile	Asn	Thr	Asn	Gly	Ser	Trp	His	Leu	Asn	Ser	Thr	Ala	Leu	Asn		
				245					250					255			
Cys	Asn	Asp	Ser	Leu	Asn	Thr	Gly	Trp	Leu	Ala	Gly	Leu	Phe	Tyr	His		
			260					265					270				
His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys	Arg		
		275					280					285					
Pro	Leu	Thr	Asp	Phe	Asp	Gln	Gly	Trp	Gly	Pro	Ile	Ser	Tyr	Ala	Asn		
	290					295					300						
Gly	Ser	Gly	Pro	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Pro	Pro	Lys		
305					310					315					320		
Pro	Cys	Gly	Ile	Val	Pro	Ala	Lys	Ser	Val	Cys	Gly	Pro	Val	Tyr	Cys		
				325					330					335			
Phe	Thr	Pro	Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Ser	Gly	Ala		
			340					345					350				
Pro	Thr	Tyr	Ser	Trp	Gly	Glu	Asn	Asp	Thr	Asp	Val	Phe	Val	Leu	Asn		
		355					360					365					
Asn	Thr	Arg	Pro	Pro	Leu	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	Met	Asn		
		370				375					380						
Ser	Thr	Gly	Phe	Thr	Lys	Val	Cys	Gly	Ala	Pro	Pro	Cys	Val	Ile	Gly		
385					390					395					400		
Gly	Ala	Gly	Asn	Asn	Thr	Leu	His	Cys	Pro	Thr	Asp	Cys	Phe	Arg	Lys		
				405					410					415			
His	Pro	Asp	Ala	Thr	Tyr	Ser	Arg	Cys	Gly	Ser	Gly	Pro	Trp	Ile	Thr		
			420					425					430				
Pro	Arg	Cys	Leu	Val	Asp	Tyr	Pro	Tyr	Arg	Leu	Trp	His	Tyr	Pro	Cys		
		435					440					445					
Thr	Ile	Asn	Tyr	Thr	Ile	Phe	Lys	Ile	Arg	Met	Tyr	Val	Gly	Gly	Val		
	450					455					460						
Glu	His	Arg	Leu	Glu	Ala	Ala	Cys	Asn	Trp	Thr	Arg	Gly	Glu	Arg	Cys		
465					470					475					480		
Asp	Leu	Glu	Asp	Arg	Asp	Arg	Ser	Glu	Leu	Ser	Pro	Leu	Leu	Leu	Thr		
				485					490					495			
Thr	Thr	Gln	Trp	Gln	Val	Leu	Pro	Cys	Ser	Phe	Thr	Thr	Leu	Pro	Ala		
			500					505					510				
Leu	Ser	Thr	Gly	Leu	Ile	His	Leu	His	Gln	Asn	Ile	Val	Asp	Val	Gln		
		515					520					525					

Tyr Leu Tyr Gly Val Gly Ser Ser Ile Ala Ser Trp Ala Ile Lys Trp
 530 535 540

Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys
 545 550 555 560

Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu Ala Ala Leu
 565 570 575

Glu Asn Leu Val Ile Leu Asn Ala Ala Ser Leu Ala Gly Thr His Gly
 580 585 590

Leu Val Ser Phe Leu Val Phe Phe Cys Phe Ala Trp Tyr Leu Lys Gly
 595 600 605

Lys Trp Val Pro Gly Ala Val Tyr Thr Phe Tyr Gly Met Trp Pro Leu
 610 615 620

Leu Leu Leu Leu Leu Ala Leu Pro Gln Arg Ala Tyr Ala
 625 630 635